

TECHNOLOGY
SYSTEMS
BRANCH

Application Serial Number

Source

Date Processed by STIC

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
E-mail: rob@wax.com or phone 703-306-4119 (R. Wax)

FOR SEQUENCE RULES INTERPRETATION, PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 2.1 e-mail help: patin2help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0
The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§ 1.821-1.1.825 effective October 1, 1996 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, i.e. Y2F-compliant Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer erred sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTEDSUGGESTED CORRECTION

SERIAL NUMBER: 04/5/6, 3/0A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3, this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/516,310A

DATE: 10/02/2001
TIME: 12:44:26

Input Set : A:\22000.0021U2.txt
Output Set : N:\CRF3\10022001\I516310A.raw

Does Not Comply
Corrected Diskette Needed

1,3-4

3 <110> APPLICANT: Lin, Yao-Zhong
4 Hawiger, Jack J.
6 <120> TITLE OF INVENTION: A Novel Method for Importing
7 Biologically Active Molecules into Cells
10 <130> FILE REFERENCE: 22000.0021U2
12 <140> CURRENT APPLICATION NUMBER: 09/516,310A
13 <141> CURRENT FILING DATE: 2000-03-01
15 <150> PRIOR APPLICATION NUMBER: 09/170,754
16 <151> PRIOR FILING DATE: 1998-10-13
18 <150> PRIOR APPLICATION NUMBER: 09/052,784
19 <151> PRIOR FILING DATE: 1998-03-31
21 <150> PRIOR APPLICATION NUMBER: 08/258,852
22 <151> PRIOR FILING DATE: 1994-06-13
24 <160> NUMBER OF SEQ ID NOS: 11
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 26
30 <212> TYPE: PRT
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <221> NAME/KEY: SITE
35 <222> LOCATION: (1)...(16)
36 <223> OTHER INFORMATION: note = Signal peptide amino acid sequence of K-FGF
38 <221> NAME/KEY: SITE
39 <222> LOCATION: (17)...(19)
40 <223> OTHER INFORMATION: note = Spacer region
42 <221> NAME/KEY: SITE
43 <222> LOCATION: (20)...(26)
44 <223> OTHER INFORMATION: note = Epitope tag
46 <400> SEQUENCE: 1
47 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Ala Pro
48 1 5 10 15
49 Ala Ala Ala Asp Gln Asn Gln Leu Met Pro
50 20 25
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 7
54 <212> TYPE: PRT
55 <213> ORGANISM: Artificial Sequence
W--> 57 <220> FEATURE:
W--> 57 <223> OTHER INFORMATION:
57 <400> SEQUENCE: 2
58 Asn Tyr Lys Lys Pro Lys Leu
59 1 5
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 26
63 <212> TYPE: PRT
64 <213> ORGANISM: Artificial Sequence

FYI: Xaa can only represent
a single amino acid

See item 11 on Error Summary
Sheet

RAW SEQUENCE LISTING

DATE: 10/02/2001

PATENT APPLICATION: US/09/516,310A

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Input Set : A:\22000.0021U2.txt

Output Set: N:\CRF3\10022001\I516310A.raw

66 <220> FEATURE:
 67 <221> NAME/KEY: SITE
 68 <222> LOCATION: (1)...(16)
 69 <223> OTHER INFORMATION: note = Signal peptide amino acid sequence of K-FGF
 71 <221> NAME/KEY: SITE
 72 <222> LOCATION: (17)...(19)
 73 <223> OTHER INFORMATION: Spacer region *Xaa can only represent a single amino acid*
 75 <221> NAME/KEY: SITE
 76 <222> LOCATION: (20)...(26)
 77 <223> OTHER INFORMATION: Nuclear localization sequence of aFGF
 79 <400> SEQUENCE: 3
 80 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 81 1 5 10 15
 82 Ala Ala Ala Asn Tyr Lys Lys Pro Lys Leu
 83 20 25
 85 <210> SEQ ID NO: 4
 86 <211> LENGTH: 28
 87 <212> TYPE: PRT
 88 <213> ORGANISM: Artificial Sequence
 90 <220> FEATURE:
 91 <221> NAME/KEY: SITE
 92 <222> LOCATION: (1)...(16)
 93 <223> OTHER INFORMATION: note = Signal peptide amino acid sequence of K-FGF
 95 <221> NAME/KEY: SITE
 96 <222> LOCATION: (17)...(19)
 97 <223> OTHER INFORMATION: note = Spacer region
 99 <221> NAME/KEY: SITE
 100 <222> LOCATION: (20)...(26)
 101 <223> OTHER INFORMATION: note = Nuclear localization sequence of aFGF
 103 <221> NAME/KEY: SITE
 104 <222> LOCATION: (27)...(28)
 105 <223> OTHER INFORMATION: note = Epitope tag
 107 <400> SEQUENCE: 4
 108 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 109 1 5 10 15
 110 Ala Ala Ala Asn Tyr Lys Lys Pro Lys Leu Met Pro
 111 20 25
 113 <210> SEQ ID NO: 5
 114 <211> LENGTH: 16
 115 <212> TYPE: PRT
 116 <213> ORGANISM: Artificial Sequence
 118 <220> FEATURE:
 119 <221> NAME/KEY: SITE
 120 <222> LOCATION: (1)...(16)
 121 <223> OTHER INFORMATION: note = Signal peptide amino acid sequence of K-FGF
 123 <400> SEQUENCE: 5
 124 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 125 1 5 10 15
 127 <210> SEQ ID NO: 6

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/516,310A

DATE: 10/02/2001
TIME: 12:44:26

Input Set : A:\22000.0021U2.txt
Output Set : N:\CRF3\10022001\I516310A.raw

128 <211> LENGTH: 41
129 <212> TYPE: PRT
130 <213> ORGANISM: Artificial Sequence *see item 11*
W--> 132 <220> FEATURE:
W--> 133 <223> OTHER INFORMATION:
132 <400> SEQUENCE: 6
133 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
134 1 5 10 15
135 Glu Ile Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr
136 20 25 30
137 Pro Gly Met Phe Ile Ala Leu Ser Lys
138 35 40
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 25
142 <212> TYPE: PRT
143 <213> ORGANISM: Artificial Sequence
W--> 145 <220> FEATURE:
W--> 145 <223> OTHER INFORMATION:
145 <400> SEQUENCE: 7
146 Glu Ile Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr
147 1 5 10 15
148 Pro Gly Met Phe Ile Ala Leu Ser Lys
149 20 25
151 <210> SEQ ID NO: 8
152 <211> LENGTH: 26
153 <212> TYPE: PRT
154 <213> ORGANISM: Artificial Sequence
W--> 156 <220> FEATURE:
W--> 156 <223> OTHER INFORMATION:
156 <400> SEQUENCE: 8
157 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
158 1 5 10 15
159 Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu
160 20 25
162 <210> SEQ ID NO: 9
163 <211> LENGTH: 26
164 <212> TYPE: PRT
165 <213> ORGANISM: Artificial Sequence
W--> 167 <220> FEATURE:
W--> 167 <223> OTHER INFORMATION:
167 <400> SEQUENCE: 9
168 Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
169 1 5 10 15
170 Val Asn Arg Lys Arg Asn Lys Leu Met Pro
171 20 25
173 <210> SEQ ID NO: 10
174 <211> LENGTH: 10
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial Sequence

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/516,310A

DATE: 10/02/2001
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Input Set : A:\22000.0021U2.txt
Output Set: N:\CRF3\10022001\I516310A.raw

W--> 178 <220> FEATURE:
W--> 178 <223> OTHER INFORMATION:
178 <400> SEQUENCE: 10
179 Val Asn Arg Lys Arg Asn Lys Leu Met Pro
180 1 5 10
182 <210> SEQ ID NO: 11
183 <211> LENGTH: 10
184 <212> TYPE: PRT
185 <213> ORGANISM: Artificial Sequence
W--> 187 <220> FEATURE:
W--> 187 <223> OTHER INFORMATION:
187 <400> SEQUENCE: 11
188 Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu
189 1 5 10

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/516,310ADATE: 10/02/2001
TIME: 12:44:27Input Set : A:\22000.0021U2.txt
Output Set: N:\CRF3\10022001\I516310A.raw

L:57 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:57 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:132 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:132 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:145 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:145 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:156 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:156 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:167 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:167 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:178 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:178 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:187 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:187 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: